radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent agents, chemiluminescent agents, magnetic particles and the like. United States Patents describing the use of such labels include, but are not limited to, Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241.

Standard techniques for cloning, DNA isolation, amplification and purification, for enzymatic reactions involving DNA ligase, DNA polymerase, restriction endonucleases and the like, and various separation techniques are those known and commonly employed by those skilled in the art. A number of standard techniques are described in Sambrook et al. (1989) *Molecular Cloning*, Second Edition, Cold Spring Harbor Laboratory, Plainview, New York; Maniatis et al. (1982) *Molecular Cloning*, Cold Spring Harbor Laboratory, Plainview, New York; Wu (ed.) (1993) *Meth. Enzymol.* **218**:Part I; Wu (ed.) (1979) *Meth Enzymol.* **68**; Wu et al. (eds.) (1983) *Meth. Enzymol.* **100** and **101**; Grossman and Moldave (eds.) *Meth. Enzymol.* **65**; Miller (ed.) (1972) *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York; Old and Primrose (1981) *Principles of Gene Manipulation*, University of California Press, Berkeley; Schleif and Wensink (1982) *Practical Methods in Molecular Biology*; Glover (ed.) (1985) *DNA Cloning* Vol. I and II, IRL Press, Oxford, UK; Hames and Higgins (eds.) (1985) *Nucleic Acid Hybridization*, IRL Press, Oxford, UK; and Setlow and Hollaender (1979) *Genetic Engineering: Principles and Methods*, Vols. 1-4, Plenum Press, New York. Abbreviations and nomenclature, where employed, are deemed standard in the field and commonly used in professional journals such as those cited herein.

Each reference cited in the present application is incorporated by reference herein to the extent that it is not inconsistent with the present Specification.

The description provided herein is for illustrative purposes, and is not intended to limit the scope of the invention as claimed herein. Any variations in the exemplified articles and/or methods which occur to the skilled artisan are intended to fall within the scope of the present invention.

Table 1A

Amino acid sequence of wild-type MerR protein from Tn21 (SEQ ID NO:2)

```
MENNLENLTIGVFAKAAGVNVETIRFYQRKGLLREPDKPYGSIRRYGEADVVRV
KFVKSAQRLGFSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMADLARMET
VLSELVCACHARKGNVSCPLIASLQGEAGLARSAMP
```

Table 1B

Nucleotide sequence encoding the wild-type MerR protein from Tn21 (SEQ ID NO:1)

```
   1  ATGGAAAATA ATTTGGAAAA CCTGACCATT GGCGTTTTTG CCAAGGCGGC
  51  CGGGGTCAAC GTGGAGACAA TCCGCTTCTA TCAGCGCAAG GGCCTGTTGC
 101  GGGAACCGGA CAAGCCTTAC GGCAGCATCC GCCGCTATGG GGAGGCGGAC
 151  GTGGTTCGGG TGAAATTCGT GAAATCGGCA CAGCGGCTGG GGTTCAGTCT
 201  GGACGAGATT GCCGAGCTGT TGCGGCTCGA CGATGGCACC CACTGCGAGG
 251  AGGCCAGCAG CCTGGCCGAA CACAAGCTCA AGGACGTGCG CGAGAAGATG
 301  GCCGACTTGG CGCGCATGGA AACCGTGCTG TCTGAACTCG TGTGCGCCTG
 351  CCATGCACGA AAGGGGAATG TTTCCTGCCC GTTGATCGCG TCACTACAGG
 401  GCGAAGCAGG CCTGGCAAGG TCAGCTATGC CTTAG
```

Table 1C

Complete amino acid sequence of the chelon protein (SEQ ID NO:4)showing novel residues not found in wild-type MerR. The last underlined residues are derived from the StrepTag vector (Genosys) and are not essential to the metal-binding domain nor do they interfere with metal binding (SEQ ID NO:3). These residues are only important for purification of the protein.

```
MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSS
GTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK
```

Table 1D

Complete 321 nucleotide DNA sequence encoding the essential 107 residues of the Chelon protein (SEQ ID NO:3). This DNA sequence does not include the sequence encoding the StrepTag portion of the protein. The DNA sequence for the StrepTag is incorporated in the Sigma-Genosys vector. Any other affinity tag or none at all (i.e. the normal wildtype sequence of the protein) could be incorporated for use in alternative protein purification schemes.

ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAA
GATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCAC
GAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGC
GAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTT
GGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATG
TTTCCTGCCCG